OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,372A

DATE: 05/02/2002
TIME: 13:00:06

Input Set : N:\Crf3\04152002\J017372.raw
Output Set: N:\CRF3\05022002\J017372A.raw

**Does Not Comply
Corrected Diskette Needed**

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 1 <110> APPLICANT: Wolfraim, Lawrence
 2        Letterio, John
 3 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
 4 <130> FILE REFERENCE: 4239-61302
 5 <140> CURRENT APPLICATION NUMBER: US/10/017,372A
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See pp 1-2, 4-5

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C--> 6 <141> CURRENT FILING DATE: 2000-10-19
 7 <150> PRIOR APPLICATION NUMBER: 60/242,292
 8 <151> PRIOR FILING DATE: 2000-10-20
 9 <160> NUMBER OF SEQ ID NOS: 39
10 <170> SOFTWARE: PatentIn version 3.1
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See item 10 on Error Summary Sheet

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12 <210> SEQ ID NO: 1
13 <211> LENGTH: 28
14 <212> TYPE: DNA
15 <213> ORGANISM: synthetic oligonucleotide
16 <400> SEQUENCE: 1                                                      28
17        ggagagatct ggtaccgaga tggcgcct
19 <210> SEQ ID NO: 2
20 <211> LENGTH: 42
21 <212> TYPE: DNA
22 <213> ORGANISM: synthetic oligonucleotide
23 <400> SEQUENCE: 2                                                      42
24        ataagaattg cggccgcttt aatcgatccc aagtgggctt gg
26 <210> SEQ ID NO: 3
27 <211> LENGTH: 48
28 <212> TYPE: DNA
29 <213> ORGANISM: synthetic oligonucleotide
30 <400> SEQUENCE: 3                                                      48
31        gactacaagg atgacgacga caaggccctg gataccaact actgcttc
33 <210> SEQ ID NO: 4
34 <211> LENGTH: 45
35 <212> TYPE: DNA
36 <213> ORGANISM: synthetic oligonucleotide
37 <400> SEQUENCE: 4                                                      45
38        cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg
40 <210> SEQ ID NO: 5
41 <211> LENGTH: 45
42 <212> TYPE: DNA
43 <213> ORGANISM: synthetic oligonucleotide
44 <400> SEQUENCE: 5                                                      45
45        gactacaagg atgacgacga caggagaaga actgctgcgt gcggc
47 <210> SEQ ID NO: 6
48 <211> LENGTH: 45
49 <212> TYPE: DNA
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5/2/02

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54 <210> SEQ ID NO: 7
55 <211> LENGTH: 8
56 <212> TYPE: PRT
57 <213> ORGANISM: synthetic oliogpeptide
58 <400> SEQUENCE: 7
59        Asp Tyr Lys Asp Asp Asp Asp Lys
60        1               5
62 <210> SEQ ID NO: 8
63 <211> LENGTH: 1197
64 <212> TYPE: DNA
65 <213> ORGANISM: fusion
66 <220> FEATURE:
67 <221> NAME/KEY: CDS
68 <222> LOCATION: (1)..(1197)
69 <223> OTHER INFORMATION:
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <222> LOCATION: (278)..(279)
73 <223> OTHER INFORMATION: Maturation cleavage site
74 <400> SEQUENCE: 8
75        atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg     48
76        Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
77        1               5                   10                  15
78        tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc     96
79        Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
80                        20                  25                  30
81        tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc    144
82        Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
83                    35                  40                  45
84        att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc    192
85        Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
86            50                  55                  60
87        cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt    240
88        Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
89        65                  70                  75                  80
90        tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag    288
91        Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
92                        85                  90                  95
93        ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta    336
94        Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
95                        100                 105                 110
96        atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc    384
97        Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
98                    115                 120                 125
99        cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg    432
100       His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
```

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101                   130              135              140              480
102      ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc
103      Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
104      145              150              155              160          528
105      aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat
106      Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
107                        165              170              175         576
108      gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca
109      Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
110                   180              185              190              624
111      ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg
112      Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
113                   195              200              205              672
114      acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc
115      Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
116                   210              215              220              720
117      tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat
118      Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
119      225              230              235              240          768
120      tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc
121      Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
122                        245              250              255         816
123      ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac
124      Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
125                   260              265              270              864
126      agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg
127      Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
128                   275              280              285              912
129      gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg
130      Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
131                   290              295              300              960
132      cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat
133      Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
134      305              310              315              320          1008
135      gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac
136      Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
137                        325              330              335         1056
138      atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac
139      Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
140                   340              345              350              1104
141      cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg
142      Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
143                   355              360              365              1152
144      ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg
145      Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
146                   370              375              380              1197
147      gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga
148      Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
149      385              390              395
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151  <210> SEQ ID NO: 9
152  <211> LENGTH: 398
153  <212> TYPE: PRT
154  <213> ORGANISM: fusion
155  <220> FEATURE:
156  <221> NAME/KEY: misc_feature
157  <222> LOCATION: (278)..(279)
158  <223> OTHER INFORMATION: Maturation cleavage site
159  <400> SEQUENCE: 9
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161       1               5                   10                  15
162       Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
163                   20                  25                  30
164       Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
165                   35                  40                  45
166       Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
167           50                  55                  60
168       Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
169       65                  70                  75                  80
170       Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
171                       85                  90                  95
172       Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
173                   100                 105                 110
174       Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
175                   115                 120                 125
176       His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
177           130                 135                 140
178       Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
179       145                 150                 155                 160
180       Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
181                       165                 170                 175
182       Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
183                   180                 185                 190
184       Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
185                   195                 200                 205
186       Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
187           210                 215                 220
188       Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
189       225                 230                 235                 240
190       Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
191                   245                 250                 255
192       Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
193                   260                 265                 270
194       Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Lys Ala Leu
195           275                 280                 285
196       Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
197           290                 295                 300
198       Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
199       305                 310                 315                 320
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200        Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
201                    325                 330                 335
202        Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
203                    340                 345                 350
204        Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
205                    355                 360                 365
206        Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
207                    370                 375                 380
208        Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
209                    385                 390                 395
211 <210> SEQ ID NO: 10
212 <211> LENGTH: 362
213 <212> TYPE: DNA
214 <213> ORGANISM: fusion
215 <400> SEQUENCE: 10
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217        aagaactgct gcgtgcggca gctctacatt gacttccgga aggacctggg ctggaagtgg   120
218        attcatgaac ccaagggctc catgccaatt tctgcctggg gccctgtccc tacatctgga   180
219        gcctagacac tcagtacagc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt   240
220        cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg   300
221        gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttcctgc aagtgcagct   360
222        ga                                                                  362
224 <210> SEQ ID NO: 11
225 <211> LENGTH: 120
226 <212> TYPE: PRT
227 <213> ORGANISM: fusionprotein
228 <220> FEATURE:
229 <221> NAME/KEY: PEPTIDE
230 <222> LOCATION: (1)..(8)
231 <223> OTHER INFORMATION: FLAG tag
232 <400> SEQUENCE: 11
233        Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu Asp Thr Asn Tyr Cys Phe
234        1                   5                   10                  15
235        Ser Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe
236                    20                  25                  30
237        Arg Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His
238                    35                  40                  45
239        Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr
240                    50                  55                  60
241        Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala
242        65                  70                  75                  80
243        Ser Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile
244                    85                  90                  95
245        Val Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met
246                    100                 105                 110
247        Ile Val Arg Ser Cys Lys Cys Ser
248                    115                 120
250 <210> SEQ ID NO: 12
251 <211> LENGTH: 1197
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The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/017,372 A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
       Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
       Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
       "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
       (OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
       (NEW RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
       (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ✓__Invalid <213>
       Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
       "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.